

Fig. 1

5' GTG GGC ATG CTG GGC AAC GCC CTG GTC TGT CAT GTC ATC TTC AAG AAC CAG CGA  
 Val Cys His Val Ile Phe Lys Asn Gln Arg

ATG CAC TCG GCC ACC AGC CTC TTC ATC GTC AAC CTG GCA GTT GCC GAC ATA ATG  
 Met His Ser Ala Thr Ser Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met

ATC ACG CTG CTC AAC ACC CCC TTC ACT TTG GTT CCC TTT GTG AAC AGC ACA TGG  
 Ile Thr Leu Leu Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp

ATA TTT GGG AAG GGC ATG TGC CAT GTC AGC CGC TTT GCC CAG TAC TGC TCA CTG  
 Ile Phe Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu

CAC GTC TCA GCA CTG ACA 3'  
 His Val Ser Ala Leu Thr

204020" 242900T

Fig. 2

5'                    9                    18                    27                    36                    45                    54  
 GAG CCA GCT GAC CTC TTC TGG AAG AAC CTG GAC TTG CCC ACC TTC ATC CTG CTC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile Leu Leu  
  
                   63                    72                    81                    90                    99                    108  
 AAC ATC CTG CCC CTC CTC ATC ATC TCT GTG GCC TAC GTT CGT GTG ACC AAG AAA  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg Val Thr Lys Lys  
  
                   117                    126                    135                    144                    153                    162  
 CTG TGG CTG TGT AAT ATG ATT GTC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu  
  
                   171                    180                    189                    198                    207                    216  
 CGG CCC AAA AAG AAG AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Arg Pro Lys Lys Lys Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe  
  
                   225                    234  
 GCC CTC TGC TGG TIG CCT CTC GAC 3'  
 --- --- --- --- --- --- --- --- ---  
Ala Leu Cys Trp Leu Pro Leu Asp

20100201 14425001

Fig. 3

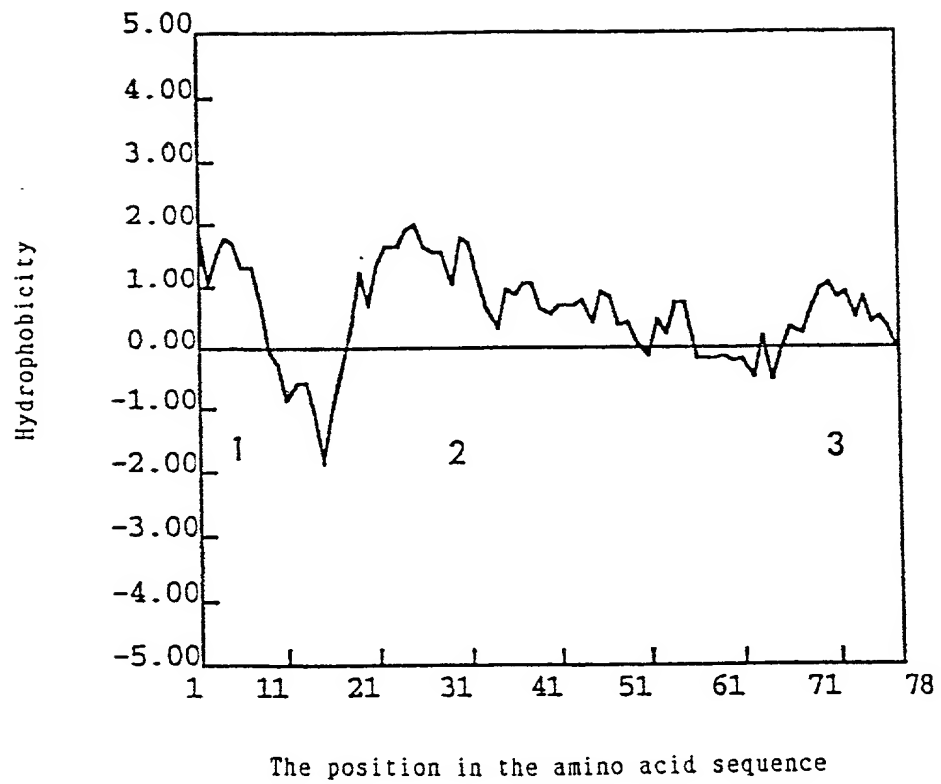


Fig. 4

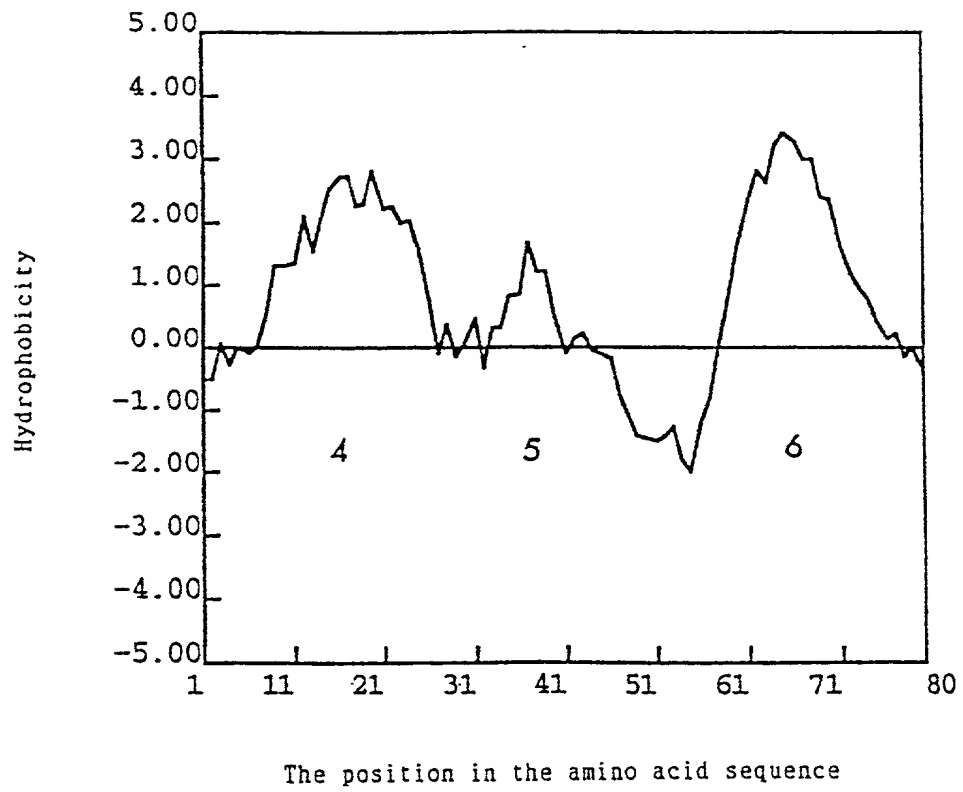


Fig. 5

p63A2 P30731	1	10	20	30	40	50	50
		VCHVIFKNQR	MHSATSLFIV	NLAVADIMTI	LLNTPFTLVR	EVNSTWIFGK	
p63A2 P30731	51	60	70	80	90	100	100
		GMCHVSRLFQ	YCSLHVSALT	LTAIAVDRHQ	VIMHPLKPRI	SITKGVITYIA	
p63A2 P30731	101	110	120	130	140	150	150
		VIWVMATFFS	LPHAICQKLF	TFKYSEDIVR	SLCLPDFPEP	ADLEWKYLDL	
p63A2 P30731	151	160	170	180	190	200	200
		PTFILLNLEP	LIISVAVVR	VTKKLWLCNM	IVDVITEQYF	ALRPKKKRTI	
p63A2 P30731	201	210	220	230	240	250	250
		KMLMLVVVL	.....	.....	.....	.....	

204020" 244900"

Fig. 6

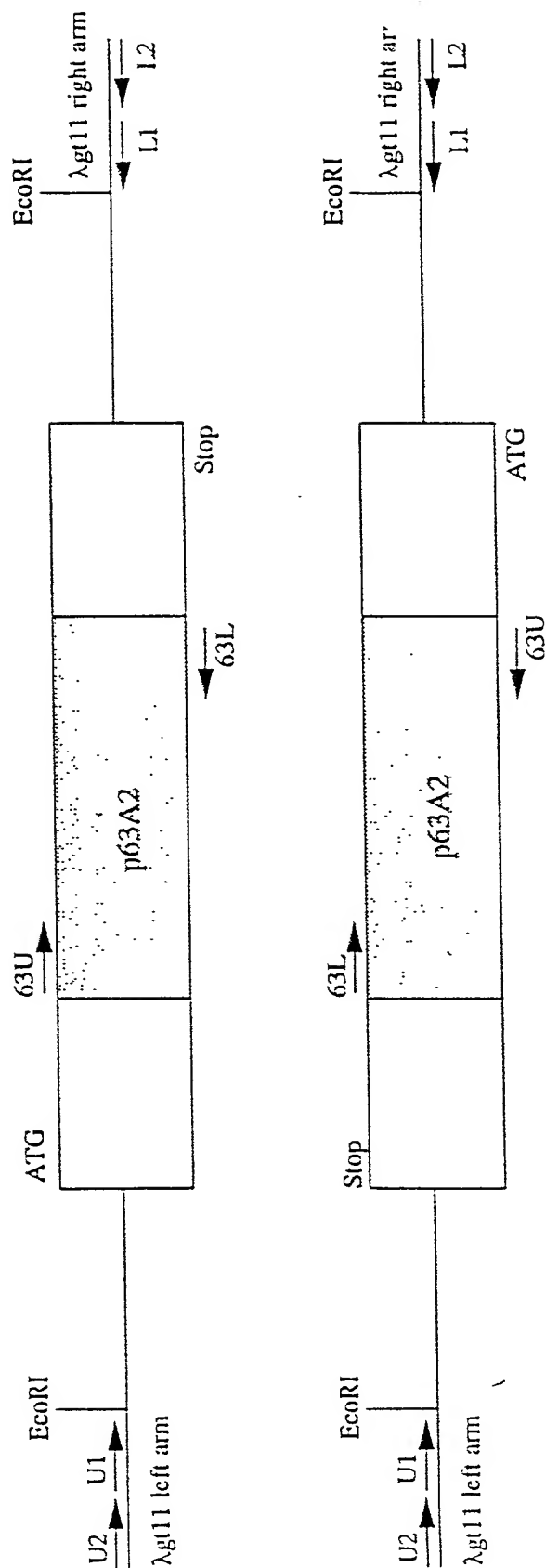
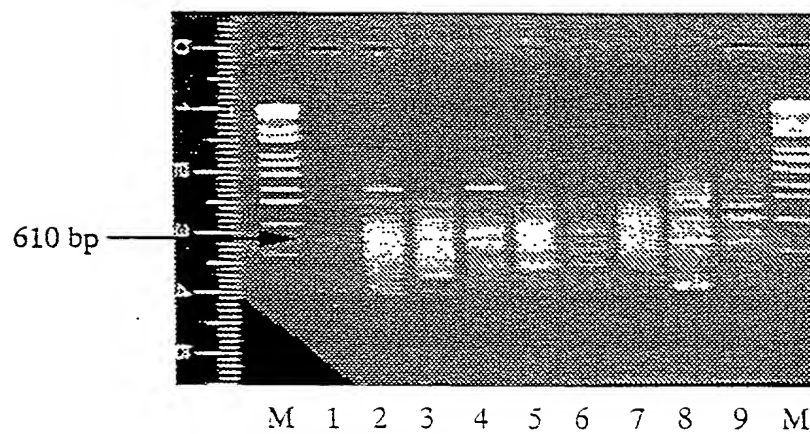


Fig. 7



M:  $\lambda$ DNA/Sty I marker

lane 1; 63U~63L

lane 2; U1~63U

lane 3; U1~63L

lane 4; U2~63U

lane 5; U2~63L

lane 6; L1~63U

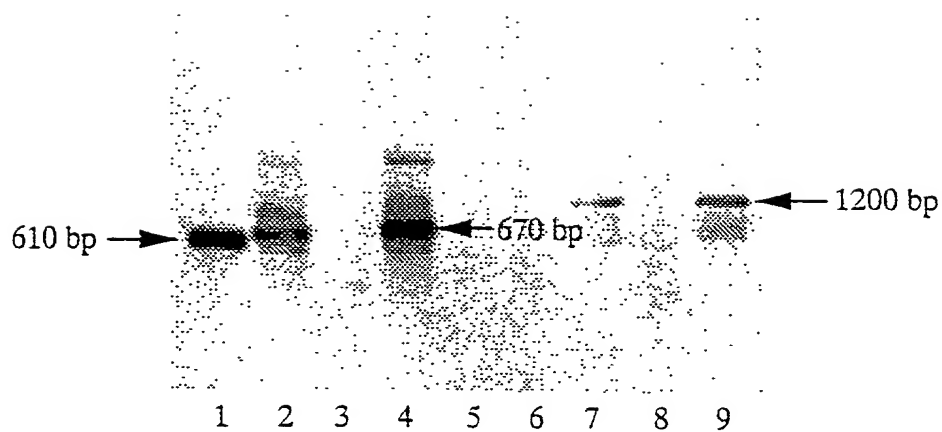
lane 7; L1~63L

lane 8; L2~63U

lane 9; L2~63L

204020" 2242900T

Fig. 8



lane 1 ; 63U~63L  
 lane 2 ; U1~63U  
 lane 3 ; U1~63L  
 lane 4 ; U2~63U  
 lane 5 ; U2~63L  
 lane 6 ; L1~63U  
 lane 7 ; L1~63L  
 lane 8 ; L2~63U  
 lane 9 ; L2~63L

204020" 2242900T



Fig. 9

63A2-5'. SEQ GGGCCCCCTTACACCCCTTTGTGATTGAGATCCGGGGTTTC-AAGGGGTGCATGATGAAG  
MUSGIR. DNA GGGCTTCCTCTGTGCCCCGTGCCCTCGCTCCAGGCTCCCTCTGTGGTGTGGACTCCTC  
130 140 150 160 170 180  
63A2-5'. SEQ GAGTAAGCCACAATGAGCAGGGCTTTACCGTGGGGTTCTGGGACTCAGCGCCCTAGCGC  
MUSGIR. DNA TAGCCCGGTGCGCTCAGC--CCCTCGCACC-CAGCCTCCAGGCACAGAGCCCGGCAGGGA  
190 200 210 220 230 240  
63A2-5'. SEQ TTCCTGCCACAAAGTTCTCCAGGGGAGGGGTGGCTCCTGCAAAATGTCCCTCACCTC  
MUSGIR. DNA GCTCAGCCC-----TTGTGCCTAGAGCTGCAGTGGCT-GGACATGAAGGTTCTCCTGTC  
250 260 270 280 290 mouse GIR  
63A2-5'. SEQ TTGCTGCTCTGTCTCCTCCCTTGGTGCGAGCCACCGAGCCCCACGAGGGCCGGGCCGAC  
MUSGIR. DNA CTGCTTCTCTTTCTTCTGTCTCAGTGCGAGCTACTGAGCAACCGCAGGTCGTCACTGAG  
300 310 320 330 340 350  
63A2-5'. SEQ 240 250 260 270 280 290  
MUSGIR. DNA GAGCAGAGCGCGGAGGGGCCCTGGCCGTGCCCAATGCCTCGCACTTCTTCTTGGAAAC  
CATCCCAGCATGGAGGCAGCCCTGACCGGGCCCAACGCCTCCTCGCACTTC---TGGGCC  
360 370 380 390 400 410  
63A2-5'. SEQ AACTACACCTTCTCCGACTGGCAGAACTTTGTGGGCAGGAGGTGCTACGGCGCTGAGTCC  
MUSGIR. DNA AACTACACTTTCTCTGACTGGCAGAACTTCGTGGGCAGGAGACGTTATGGGGCCGAGTCC  
420 430 440 450 460 470  
63A2-5'. SEQ 360 370 380  
MUSGIR. DNA CAGAACCCACGGTGAAAGCCCTGCTC  
CAGAACCCACGGTGAAAGCACTGCTC  
480 490 500

204020" 424900T

[illegible][illegible]

Fig. 11

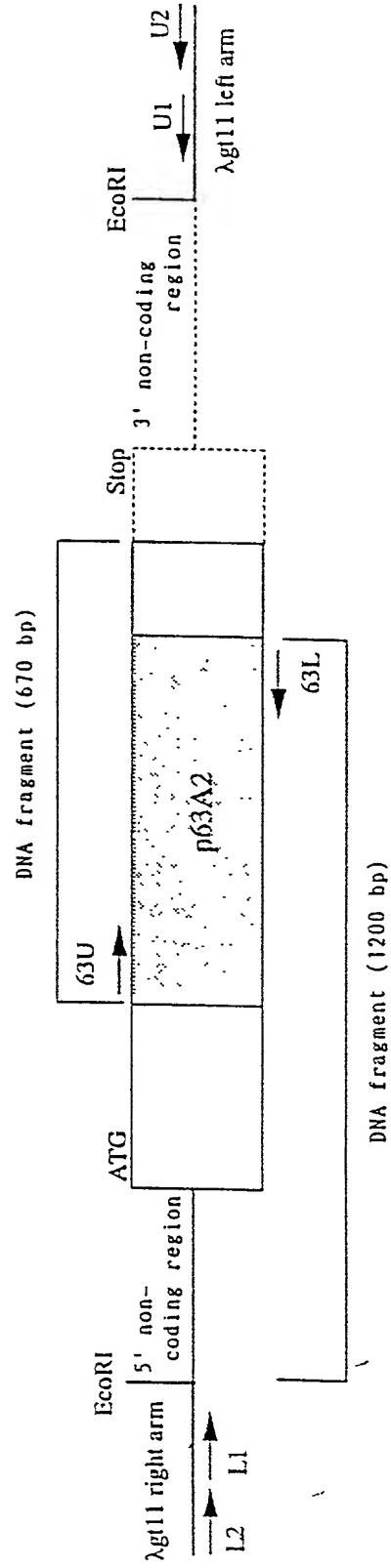
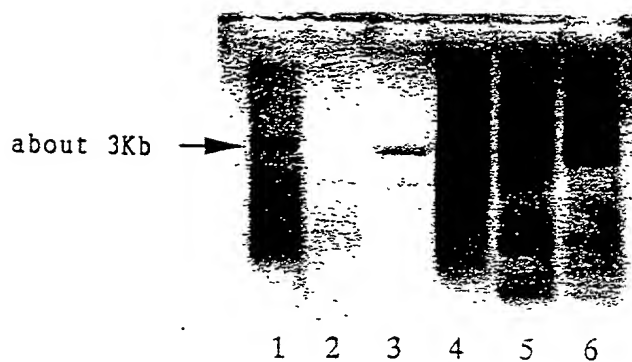




Fig. 13

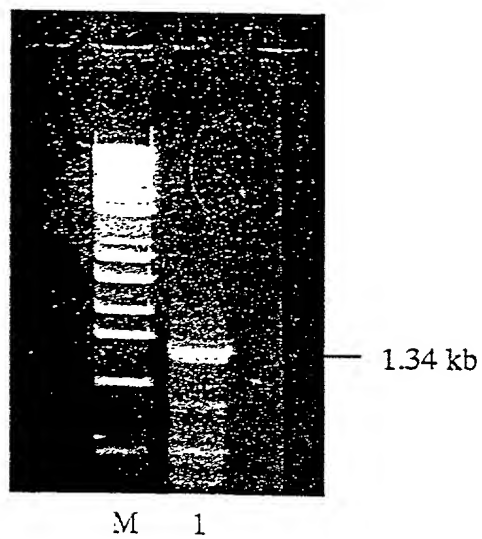


lane 1 ; 63U~Anchor Primer	Primary PCR
lane 2 ; 63-6~Anchor Primer	
lane 3 ; 63-7~Anchor Primer	
lane 4 ; 63-6~Anchor Primer	Secondary PCR
lane 5 ; 63-7~Anchor Primer	
lane 6 ; 63-8~Anchor Primer	

204020" 2242900T

		10	20	30	40	50	60
63A2-3'. seq		CCCTCTGCTGGTTCC	CCCTCAACTGCTACGTCCTCCTCTGTCCAGCAAGGTCATCCGCA				
MUSGIR. DNA		CCCTCTGCTGGTTCC	CCTCTCAACTGCTATGTCCTCCTCTTGTCCAGCAAGGCCATCCACA				
		1190	1200	1210	1220	1230	1240
	70	80	90	100	110	120	
63A2-3'. seq		CCAACAATGCCCTCTACTTTGCCTTCCACTGGTTTGCCATGAGCAGCACCTGCTATAACC					
MUSGIR. DNA		CCAACAATGCCCTCTACTTTGCCTTCCACTGGTTTGCCATGAGCAGTACTTGTATAACC					
		1250	1260	1270	1280	1290	1300
	130	140	150	160	170	180	
63A2-3'. seq		CCTTCATATACTGCTGGCTGAACGAGAACTTCAGGATTGAGCTAAAGGCATTACTGAGCA					
MUSGIR. DNA		CCTTCATCTACTGCTGGCTCAATGAGAACTTTAGGGTTGAGCTTAAGGCATTGCTGAGCA					
		1310	1320	1330	1340	1350	1360
	190	200	210	220	230	240	
63A2-3'. seq		TGTGTCAAAGACCTCCCAAGCCTCAGGAGGACAGGCCACCCTCCCAGTTCCTTCCTTCA					
MUSGIR. DNA		TGTGCCAAAGGCCACCCAAGCCGACAGGAAGACAGGCTACCCTCCCAGTTCCTTCCTTCA					
		1370	1380	1390	1400	1410	1420
	250	260	270	280	290	300	
63A2-3'. seq		GGGTGGCCTGGACAGAGAAGAATGATGGCCAGAGGGCTCCCCTTGCCAATAACCTCCTGC					
MUSGIR. DNA		GGGTGGCATGGACAGAGAAGAGCCATGGTGGGAGGGCTCCACTACCTAATCACCCTTGC					
		1430	1440	1450	1460	1470	1480
	310	320	330	340	350	360	
63A2-3'. seq		CCACCTCCCAACTCCAGTCTGGGAAGACAGACCTGTCTGTGGAACCCATTGTGACGA					
MUSGIR. DNA		CCTCTTCCAGATCCAGTCTGGGAAGACAGATCTGTCTGTGGAACCCGTTGTGGCCA					
		1490	1500	1510	1520	1530	1540
	370	380	390	400	410		
63A2-3'. seq		TGAGT <u>AG</u> AAGAGGTTGGGAAGAGGGAGTGGGAGGGGTCTGT-CTC-CAC-CTGAGGCAG					
MUSGIR. DNA		TGAGT <u>AG</u> GGAAGGCT-GGAAGTTGGTGGGGAGGGTTCTTTCCTCTCACAATTGACCAG					
mouse GIR stop codon		1550	1560	1570	1580	1590	1600
	420	430	440	450	460	470	
63A2-3'. seq		GGA--AAGAGAG-CCTATTCTCACACATGATC-TTCAGAGTGCTGGAAACACACTCCTGC					
MUSGIR. DNA		ACACTAACAGAGTTGGAAAGTAACACAGAAGCAGTGAGA-TGCTTGGGTTCTAGGAACC					
		1610	1620	1630	1640	1650	1660
	480	490					
63A2-3'. seq		AGAAGCTGTAGGACTCTTGAAT					
MUSGIR. DNA		TGTCCAGCCCCATCTGATTTC					
		1670	1680				

Fig. 15



M ;  $\lambda$  / StyI  
lane 1 ; Whole Brain

204020" 442900T

5'	ATG	GTC	CCT	CAC	CTC	TTG	CTG	CTC	TGT	CTC	CTC	CCC	TTG	GTG	CGA	GCC	ACC	GAG
	Met	Val	Pro	His	Leu	Leu	Leu	Leu	Cys	Leu	Leu	Pro	Leu	Val	Arg	Ala	Thr	Glu
	CCC	CAC	GAG	GGC	CGG	GCC	GAC	GAG	CAG	AGC	GCG	GAG	GCG	GCC	CTG	GCC	GTG	CCC
	Pro	His	Glu	Gly	Arg	Ala	Asp	Glu	Gln	Ser	Ala	Glu	Ala	Ala	Leu	Ala	Val	Pro
	AAT	GCC	TCG	CAC	TTC	TTC	TCT	TGG	AAC	AAC	TAC	ACC	TTC	TCC	GAC	TGG	CAG	AAC
	Asn	Ala	Ser	His	Phe	Phe	Ser	Trp	Asn	Asn	Tyr	Thr	Phe	Ser	Asp	Trp	Gln	Asn
	TTT	GTG	GGC	AGG	AGG	CGC	TAC	GGC	GCT	GAG	TCC	CAG	AAC	CCC	ACG	GTG	AAA	GCC
	Phe	Val	Gly	Arg	Arg	Arg	Tyr	Gly	Ala	Glu	Ser	Gln	Asn	Pro	Thr	Val	Lys	Ala
	CTG	CTC	ATT	GTG	GCT	TAC	TCC	TTC	ATC	ATT	GTC	TTC	TCA	CTC	TTT	GGC	AAC	GTC
	Leu	Leu	Ile	Val	Ala	Tyr	Ser	Phe	Ile	Ile	Val	Phe	Ser	Leu	Phe	Gly	Asn	Val
	CTG	GTC	TGT	CAT	GTC	ATC	TTC	AAG	AAC	CAG	CGA	ATG	CAC	TCG	GCC	ACC	AGC	CTC
	Leu	Val	Cys	His	Val	Ile	Phe	Lys	Asn	Gln	Arg	Met	His	Ser	Ala	Thr	Ser	Leu
	TTC	ATC	GTC	AAC	CTG	GCA	GTT	GCC	GAC	ATA	ATG	ATC	ACG	CTG	CTC	AAC	ACC	CCC
	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Asp	Ile	Met	Ile	Thr	Leu	Leu	Asn	Thr	Pro
	TTC	ACT	TTG	GTT	CGC	TTT	GTG	AAC	AGC	ACA	TGG	ATA	TTT	GGG	AAG	GGC	ATG	TGC
	Phe	Thr	Leu	Val	Arg	Phe	Val	Asn	Ser	Thr	Trp	Ile	Phe	Gly	Lys	Gly	Met	Cys
	CAT	GTC	AGC	CGC	TTT	GCC	CAG	TAC	TGC	TCA	CTG	CAC	GTC	TCA	GCA	CTG	ACA	CTG
	His	Val	Ser	Arg	Phe	Ala	Gln	Tyr	Cys	Ser	Leu	His	Val	Ser	Ala	Leu	Thr	Leu
	ACA	GCC	ATT	GCG	GTG	GAT	CGC	CAC	CAG	GTC	ATC	ATG	CAC	CCC	TTG	AAA	CCC	CGG
	Thr	Ala	Ile	Ala	Val	Asp	Arg	His	Gln	Val	Ile	Met	His	Pro	Leu	Lys	Pro	Arg
	ATC	TCA	ATC	ACA	AAG	GGT	GTC	ATC	TAC	ATC	GCT	GTC	ATC	TGG	ACC	ATG	GCT	ACG
	Ile	Ser	Ile	Thr	Lys	Gly	Val	Ile	Tyr	Ile	Ala	Val	Ile	Trp	Thr	Met	Ala	Thr
	TTC	TTT	TCA	CTC	CCA	CAT	GCT	ATC	TGC	CAG	AAA	TTA	TTT	ACC	TTC	AAA	TAC	AGT
	Phe	Phe	Ser	Leu	Pro	His	Ala	Ile	Cys	Gln	Lys	Leu	Phe	Thr	Phe	Lys	Tyr	Ser
	GAG	GAC	ATT	GTG	CGC	TCC	CTC	TGC	CTG	CCA	GAC	TTC	CCT	GAG	CCA	GCT	GAC	CTC
	Glu	Asp	Ile	Val	Arg	Ser	Leu	Cys	Leu	Pro	Asp	Phe	Pro	Glu	Pro	Ala	Asp	Leu

204020 " 242900T



Fig. 17

711	720	729	738	747	756
TTC TGG AAG TAC CTG GAC TTG GCC ACC TTC ATC CTG CTC TAC ATC CTG CCC CTC					
Phe Trp Lys Tyr Leu Asp Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu					
765	774	783	792	801	810
CTC ATC ATC TCT GTG GCC TAC GCT CGT GTG GCC AAG AAA CTG TGG CTG TGT AAT					
Leu Ile Ile Ser Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn					
819	828	837	846	855	864
ATG ATT GGC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG CGG CGC AAA AAG AAG					
Met Ile Gly Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu Arg Arg Lys Lys Lys					
873	882	891	900	909	918
AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT GCC CTC TGC TGG TTC					
Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe Ala Leu Cys Trp Phe					
927	936	945	954	963	972
CCC CTC AAC TGC TAC GTC CTC CTC CTG TCC AGC AAG GTC ATC CGC ACC AAC AAT					
Pro Leu Asn Cys Tyr Val Leu Leu Leu Ser Ser Lys Val Ile Arg Thr Asn Asn					
981	990	999	1008	1017	1026
GCC CTC TAC TTT GCC TTC CAC TGG TTT GCC ATG AGC AGC ACC TGC TAT AAC CCC					
Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser Ser Thr Cys Tyr Asn Pro					
1035	1044	1053	1062	1071	1080
TTC ATA TAC TGC TGG CTG AAC GAG AAC TTC AGG ATT GAG CTA AAG GCA TTA CTG					
Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe Arg Ile Glu Leu Lys Ala Leu Leu					
1089	1098	1107	1116	1125	1134
AGC ATG TGT CAA AGA CCT CCC AAG CCT CAG GAG GAC AGG CCA CCC TCC CCA GTT					
Ser Met Cys Gln Arg Pro Pro Lys Pro Gln Glu Asp Arg Pro Pro Ser Pro Val					
1143	1152	1161	1170	1179	1188
CCT TCC TTC AGG GTG GCC TGG ACA GAG AAG AAT GAT GGC CAG AGG GCT CCC CTT					
Pro Ser Phe Arg Val Ala Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu					
1197	1206	1215	1224	1233	1242
GCC AAT AAC CTC CTG CCC ACC TCC CAA CTC CAG TCT GGG AAG ACA GAC CTG TCA					
Ala Asn Asn Leu Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser					
1251	1260	1269			
TCT GTG GAA CCC ATT GTG ACG ATG AGT TAG 3'					
Ser Val Glu Pro Ile Val Thr Met Ser ***					

204020-4900T 1006747-020402

Fig. 18

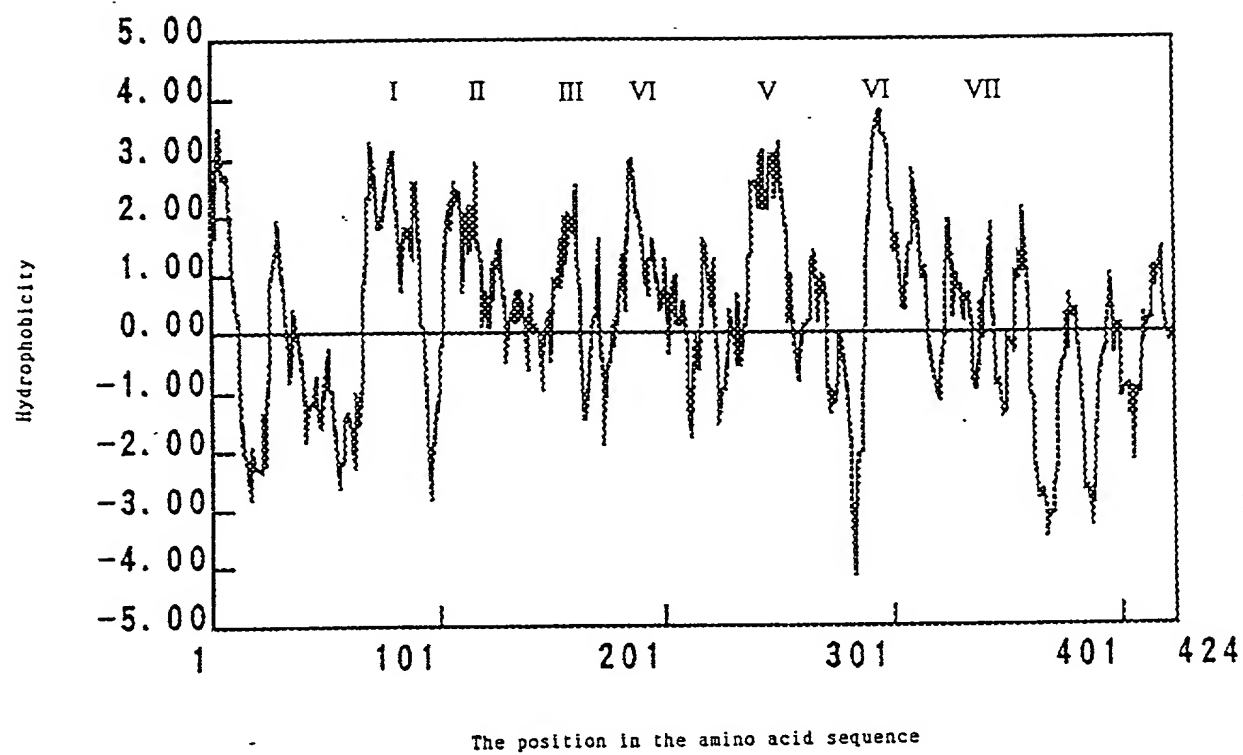


Fig. 19

63A2. AMI	1	10 20 30 40 50					50
		M-VPHLLLLC	LLPLVRATEP	HEGRADEQSA	EAALAVPNAS	HFESWNNYTF	
MUSGIR. AMI	1	MKVPPVLLLF	LLSSVRATEQ	PQVYTEHPSM	EAALTGPNAS	SHF-WANNYTF	50
63A2. AMI	51	60 70 80 90 100					100
		SDWQNFVGRR	RYGAESQNP	VKALLIVAYS	FIIVFSLFGN	VLVCHVIFKN	
MUSGIR. AMI	51	SDWQNFVGRR	RYGAESQNP	VKALLIVAYS	FIIVFSLFGN	VLVCHVIFKN	100
63A2. AMI	101	110 120 130 140 150					150
		QRMHSATSLF	IVNLAVADIM	ITLLNTPFTL	VRFVNSTWIF	GKGMCHVSRF	
MUSGIR. AMI	101	QRMHSATSLF	IVNLAVADIM	ITLLNTPFTL	VRFVNSTWIF	GKGMCHVSRF	150
63A2. AMI	151	160 170 180 190 200					200
		AQYCSLHVSA	LTLTAIIVDR	HQVIMHPLKP	RISITKGVIV	IAVIWTMATE	
MUSGIR. AMI	151	AQYCSLHVSA	LTLTAIIVDR	HQVIMHPLKP	RISITKGVIV	IAVIWTMATE	200
63A2. AMI	201	210 220 230 240 250					250
		FSLPHAICQK	LFTFKYSEDI	VRSLCLPDFP	EPADLFWKYL	OLATFILLYL	
MUSGIR. AMI	201	FSLPHAICQK	LFTFKYSEDI	VRSLCLPDFP	EPADLFWKYL	OLATFILLYL	250
63A2. AMI	251	260 270 280 290 300					300
		LPLIISVAY	ARVAKKLWLC	NMIGDVTTEQ	YALRRKKKK	TIKMLMEVVV	
MUSGIR. AMI	251	LPLIISVAY	ARVAKKLWLC	NTIGDVTTEQ	YALRRKKKT	TYKMLVLVVV	300
63A2. AMI	301	310 320 330 340 350					350
		LFALCWFLN	CYVLLSSKY	IRTNALYFA	FHWFAMSSTC	YNPFIYCWLN	
MUSGIR. AMI	301	LFALCWFLN	CYVLLSSKA	IRTNALYFA	FHWFAMSSTC	YNPFIYCWLN	350
63A2. AMI	351	360 370 380 390 400					400
		ENFRVELKAL	LSMCORPPKP	QEDR PSPVP	SFRVAWTEKN	DGRAPLANH	
MUSGIR. AMI	351	ENFRVELKAL	LSMCORPPKP	QEDR PSPVP	SFRVAWTEKS	HGRAPLANH	400
63A2. AMI	401	410 420 430 440 450					450
		LLPTSQLQSG	KTDLSSVEPI	VTMS*.....	.....	.....	
MUSGIR. AMI	401	HLPSQIQSG	KTDLSSVEPI	VAMS*.....	.....	.....	450

204020" 249002